IN THE CLAIMS:

Please **amend** claims 1-4, 6-11, 13, 16 and 41-44 as follows:

1.   (Currently Amended) A method for determining a probability for one or more states for a **selected** nucleotide in a nucleic acid sequence, comprising:

a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in said nucleic acid sequence;

b) determining transition probabilities for each of said states for nucleotides within said nucleic acid sequence following said initial oligonucleotide;

c) ~~determining a probability for said nucleic acid sequence for each of said states~~ **using said initial oligonucleotide probability and said transition probabilities to determine a plurality of nucleic acid sequence probabilities, said plurality comprising a nucleic acid sequence probability corresponding to each of said states for said selected nucleotide**; and,

d) **applying a bias function to said plurality of nucleic acid sequence probabilities, to determine** ~~determining~~ a probability for each of said states for said **selected** nucleotide**, wherein said bias function does not have the same value in all of said states for said selected nucleotide** ~~based upon said probability of said nucleic acid sequence and a bias~~.

2.   (Currently Amended) The method of claim 1, wherein said probability for each of said states for said **selected** nucleotide is determined using an inhomogeneous Markov model having eight states, wherein said eight states are: first reading frame positive strand (1+); second reading frame positive strand (2+); third reading frame positive strand (3+); first reading frame negative strand (1-); second reading frame negative strand (2-); third reading frame negative strand (3-); noncoding positive strand (N+); and, noncoding negative strand (N-).

3. (Currently Amended) The method of claim 2, wherein said probability for each of said eight states for said **selected** nucleotide ~~in step e)~~ is determined using the equation

$$P(f|S) = \frac{\phi(f) \cdot P_f \cdot P_f(S)}{\displaystyle\sum_{i \in \{1+,2+,3+,N+,1-2-,3-,N-\}} \phi(f) \cdot P_i \cdot P_i(S)}$$

4. (Currently Amended) The method of claim 1, wherein said **selected** nucleotide is the middle nucleotide in said nucleic acid sequence.

5. (Original) The method of claim 1, wherein said nucleic acid sequence is part of a longer nucleic acid sequence.

6. (Currently Amended) The method of claim 1, wherein said bias **function has a value** ~~is~~ between 0.0 and 0.9, or greater than 1.1, **in one or more of said states for said selected nucleotide**.

7. (Currently Amended) A method for determining a probability for one or more states for a **selected** nucleotide in a nucleic acid sequence, comprising:

a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in said nucleic acid sequence;

b) determining transition probabilities for each of said states for nucleotides within said nucleic acid sequence following said initial oligonucleotide;

c) ~~determining a probability for said nucleic acid sequence for each of said states~~ **using said initial oligonucleotide probability and said transition probabilities to determine a plurality of nucleic acid sequence probabilities, said plurality comprising a nucleic acid sequence probability corresponding to each of said states for said selected nucleotide**; and,

d) determining a probability for each of said states for said **selected** nucleotide, wherein said determining a probability for each of said states ~~is capable of accepting~~

accepts a bias **function, and wherein said bias function does not have the same value in all of said states for said selected nucleotide**.

8.   (Currently Amended) A method for determining a probability for each of one or more states for more than one **selected** nucleotide in a nucleic acid sequence comprising:

a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in a window of a first **selected** nucleotide;

b) determining transition probabilities for each of said states for nucleotides within said window following said initial oligonucleotide;

c) **using said initial oligonucleotide probability and said transition probabilities to determine a plurality of window probabilities, wherein said plurality comprises a window probability corresponding to each of said states for said selected nucleotide**; ~~determining a probability for said window for each of said states~~;

d) **applying a bias function to said plurality of window probabilities, to determine** ~~determining~~ a probability for each of said states for said **selected** nucleotide, **wherein said bias function does not have the same value in all of said states for said selected nucleotide** ~~based upon said probability for said window and a bias~~; and,

e) repeating steps a) through d) for each remaining **selected** nucleotide in said nucleic acid sequence.

9.   (Currently Amended) The method of claim 8, wherein said more than one **selected** nucleotide are contiguous, and step e) is performed sequentially from said first **selected** nucleotide to a last **selected** nucleotide.

10.   (Currently Amended) The method of claim 9, wherein said probability for each of said states for said more than one **selected** nucleotide is determined using an inhomogeneous Markov model having eight states, wherein said eight states are: first reading frame positive strand (1+); second reading frame positive strand (2+); third

reading frame positive strand (3+); first reading frame negative strand (1-); second reading frame negative strand (2-); third reading frame negative strand (3-); noncoding positive strand (N+); and, noncoding negative strand (N-).

11.   (Currently Amended) The method of claim 10, wherein said probability for each of said states for said more than one **selected** nucleotide is determined using the equation

$$P(f|S) = \frac{\phi(f) \cdot P_f \cdot P_f(S)}{\sum_{i \in \{1+,2+,3+,N+,1-2-,3-,N-\}} \phi(f) \cdot P_i \cdot P_i(S)}$$

12.   (Original) The method of claim 8, wherein said nucleic acid sequence is part of a longer nucleic acid sequence.

13.   (Currently Amended) The method of claim 8, wherein each **selected** nucleotide in said more than one **selected** nucleotide is the middle nucleotide in its own window.

14.   (Original) The method of claim 8, further comprising:

f) extending said nucleic acid sequence if said window extends beyond either end of said nucleic acid sequence, wherein said extending is accomplished by copying nucleotides from an end of said nucleic acid sequence at which said window is located to produce a copied nucleotide sequence, and adding said copied nucleotide sequence to said end.

15.   (Previously presented) The method of claim 8, wherein said window has a length of about 75 to about 125 nucleotides.

16.   (Currently amended) The method of claim 8, wherein said bias **function has a value** ~~is~~ between 0.0 and 0.9**,** or greater than 1.1**, in one or more of said states for said selected nucleotide.**

17. – 40. (Cancelled)

41.   (Currently Amended) A method for determining a probability for one or more states for a **selected** nucleotide in a nucleic acid sequence, comprising determining a probability for each of said states for said **selected** nucleotide **by applying a bias function to** ~~based upon~~ a probability of said nucleic acid sequence ~~and a bias~~.

42.   (Currently amended) A method for determining a probability for each of one or more states for more than one nucleotide in a nucleic acid sequence comprising:

        a) determining a probability for each of said states for a first **selected** nucleotide in said nucleic acid sequence ~~based upon~~ **by applying a bias function to** a probability of a window in which said first nucleotide is located ~~and a bias~~; and,

        b) repeating step a) for the remaining nucleotides in said nucleic acid sequence.

43.   (Currently amended) A program storage device readable by a machine, tangibly embodying a program of instructions executable by a machine to perform method steps to determine a probability for each of one or more states for a **selected** nucleotide in a nucleic acid sequence, said method steps comprising:

        a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in said nucleic acid sequence;

        b) determining transition probabilities for each of said states for nucleotides within said nucleic acid sequence following said initial oligonucleotide;

c) **using said initial oligonucleotide probability and said transition probabilities to determine a plurality of nucleic acid sequence probabilities, wherein said plurality comprises a nucleic acid sequence probability corresponding to each of said states for said selected nucleotide** ~~determining a probability for said nucleic acid sequence for each of said states~~; and,

d) **applying a bias function to said plurality of nucleic acid sequence probabilities, to determine** ~~determining~~ a probability for each of said states for said nucleotide**, wherein said bias function does not have the same value in all of said states for said selected nucleotide** ~~based upon said probability of said nucleic acid sequence and a bias~~.

44.   (Currently amended) A program storage device readable by a machine, tangibly embodying a program of instructions executable by a machine to perform method steps to determine a probability for one or more states for more than one nucleotide in a nucleic acid sequence, said method steps comprising:

a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in a window of a first **selected** nucleotide;

b) determining transition probabilities for each of said states for nucleotides within said window following said initial oligonucleotide;

c) **using said initial oligonucleotide probability and said transition probabilities to determine a plurality of window probabilities, wherein said plurality comprises a window probability corresponding to each of said states for said selected nucleotide** ~~determining a probability for said window for each of said states~~;

d) **applying a bias function to said plurality of window probabilities, to determine** ~~determining~~ a probability for each of said states for said nucleotide**, wherein said bias function does not have the same value in all of said states for said selected nucleotide** ~~based upon said probability for said window and a bias~~; and,

e) repeating steps a) through d) for each remaining nucleotide in said nucleic acid sequence.